

Fig. 1(A)

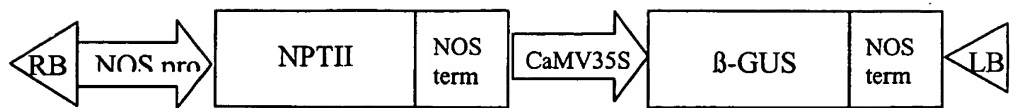


Fig. 1(B)

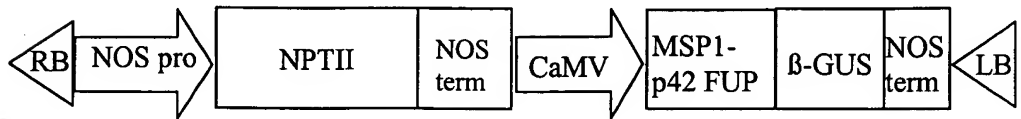


Fig. 1(C)

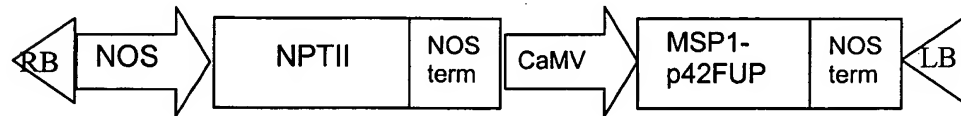
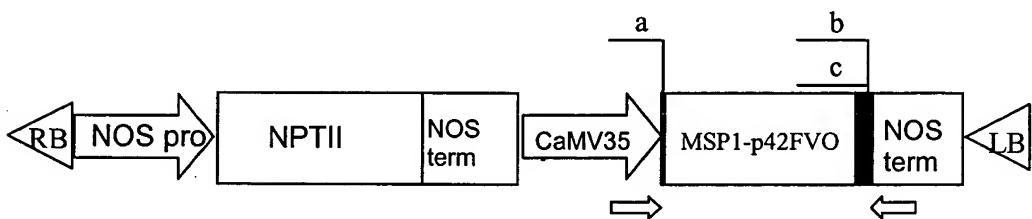


Fig. 1(D)



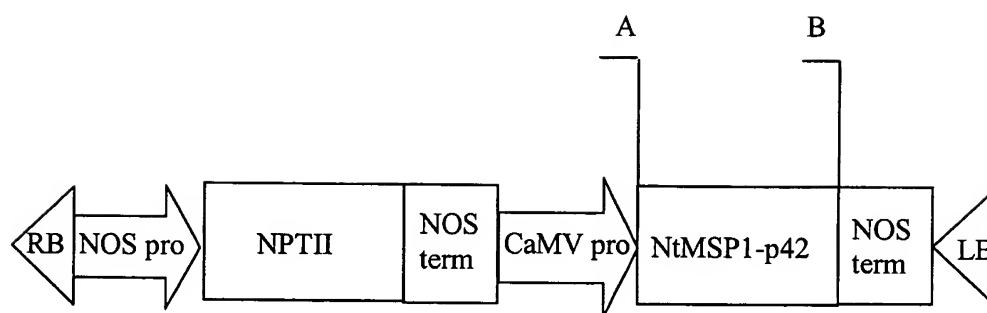


Fig. 2

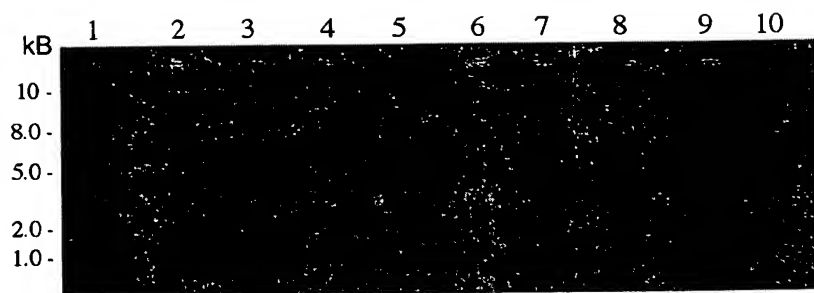


Fig. 3(A)

← MSP1-p42a
← MSP1-p42b

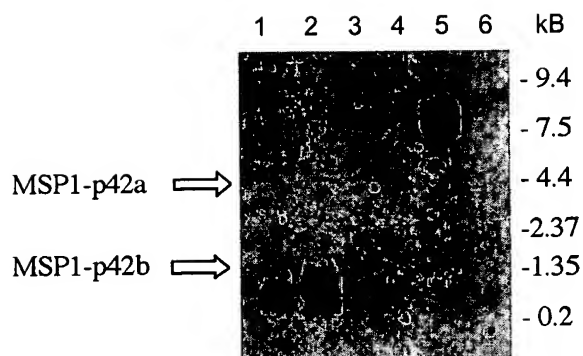


Fig. 3(B)

1009514-0140

Fig 4(A)

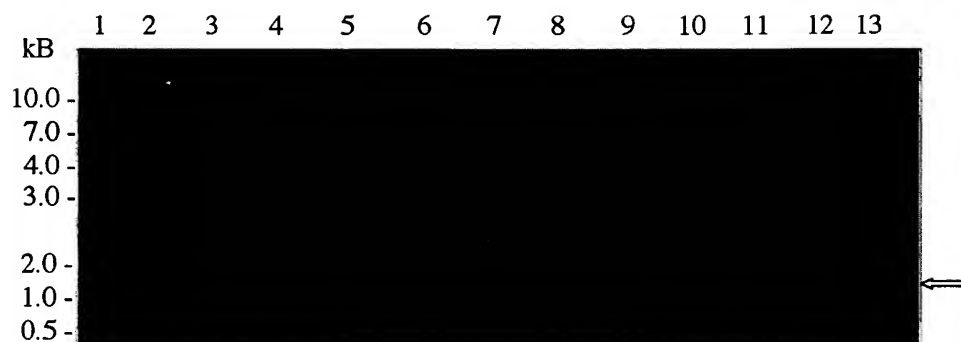
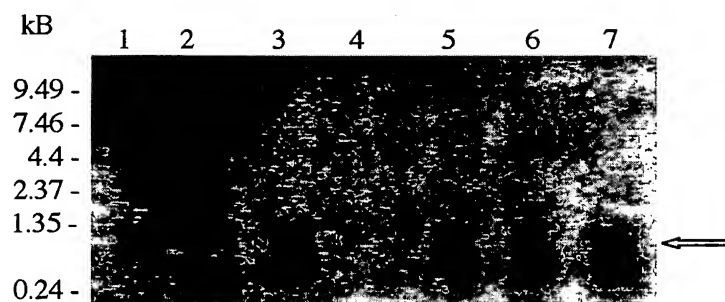


Fig. 4(B)



20170414-153500F

Fig. 5(A)

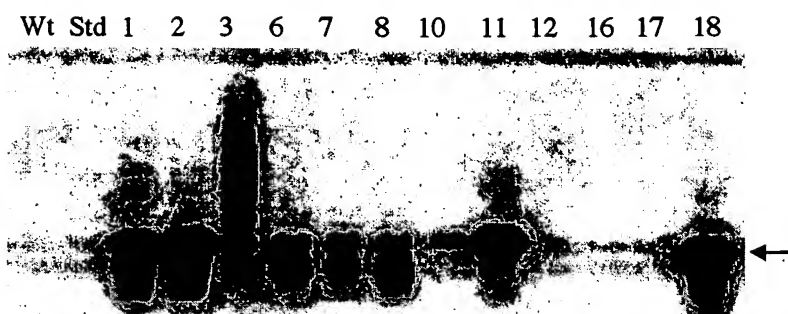
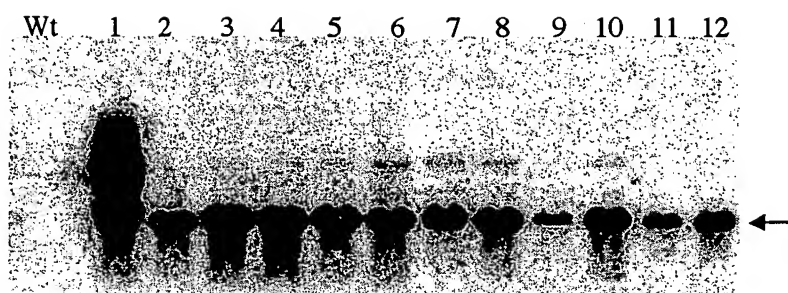


Fig. 5(B)



20160114-091102

Fig 6(A)

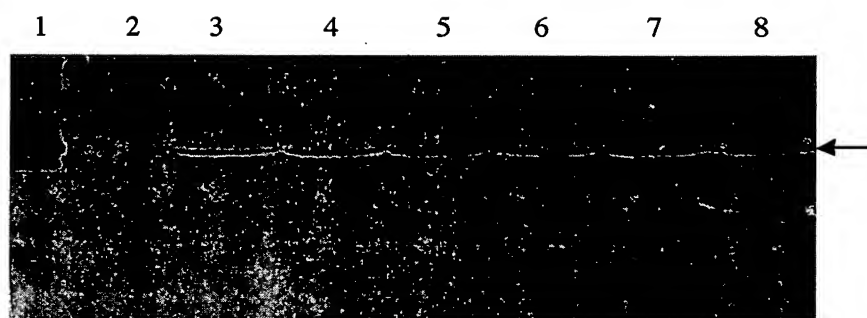
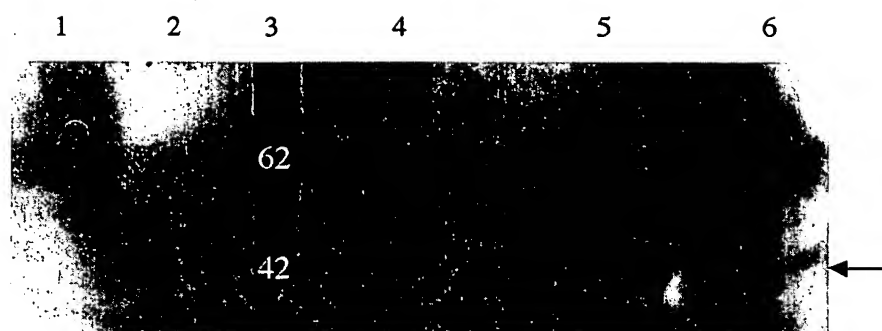


Fig. 6(B)

10098544-034402

Fig. 7(A)

MSP1.p42 FUP

401 AAAATGATATTAAAT TTGCACAGGA AGGTATAAG TTATTATGAAAAGGTT
601 AACATTGAGAC CTTATACAATAAC TTAGTTAATAAAAT TGACGATTACTT
951 TCCAGAAAAT TCTGGATGTTTCAGAC ATTTAGATGAAAG AGAAGAATGTA

MSP1.p42FVO

181 AATTTCAAAATG TTTTAGAATCAGATTTA ATTCCATATAAAG ATTTA
230 ACATCAAGTAATT ATGTTGTCAAAGATCCA TATAAATTTCTTAATAAA
277 GAAAAAAGAGA TAAATTCTTAAGCAGTTA TAATTATATTAAGGATTC

Fig. 7(B)

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2017-07-14 14:09:10

1006544-034400

A E F D N I L S D N I L S G F E N E	18
GCC GAA TTC GAC AAC ATC CTC AGT GAC AAC ATC CTC AGT GGC TTC GAG AAC GAG	54
Y D V I Y L K P L A G V Y R S L K K	36
TAC GAC GTA ATC TAC CTA AAG CCC CTT GCC GGT GTC TAC CGT TCA TTG AAG AAA	108
Q I E K N I F T F N L N L N D I L N	54
CAG ATA GAA AAG AAT ATT TTC ACG TTC AAC CTC AAC CTA AAT GAC ATC CTC AAC	162
S R L K K R K Y F L D V L E S D L M	72
TCG CGC CTC AAG AAG CGA AAA TAC TTC CTC GAC GTG TTG GAA TCC GAC CTT ATG	216
Q F K H I S S N E Y I I E D S F K L	90
CAA TTC AAG CAC ATT AGC TCT AAC GAG TAC ATC ATA GAG GAC AGC TTC AAG CTC	270
L N S E Q K N T L L K S Y K Y I K E	108
TTG AAT TCA GAA CAG AAG AAC ACC CTC CTA AAG TCC TAC AAA TAC ATT AAG GAG	324
S V E N D I K F A Q E G I S Y Y E K	126
TCT GTT GAG AAC GAC ATC AAG TTC GCC CAG GAA GGA ATT AGC TAC TAT GAG AAA	378
V L A K Y K D D L E S I K K V I K E	144
GTC CTG GCT AAA TAC AAG GAC GAC TTG GAA AGC ATT AAG AAG GTA ATC AAA GAA	432
E K E K F P S S P P T T P P S P A K	162
GAG AAG GAA AAG TTT CCG AGC TCT CCA CCC ACA ACT CCC CCA TCG CCT GCA AAG	486
T D E Q K K E S K F L P F L T N I E	180
ACC GAC GAG CAG AAA AAA GAA AGT AAG TTC CTT CCA TTC CTC ACC AAC ATC GAA	540
T L Y N N L V N K I D D Y L I N L K	198
ACT CTA TAT AAC AAC CTG GTG AAC AAG ATT GAT GAC TAC TTA ATC AAC TTG AAG	594
A K I N D C N V E K D E A H V K I T	216
GCG AAA ATT AAT GAC TGT AAC GTC GAA AAG GAT GAA GCC CAC GTT AAG ATC ACC	648
K L S D L K A I D D K I D L F K N H	234
AAG CTT TCC GAT CTC AAA GCC ATC GAC GAT AAG ATT GAC CTG TTT AAG AAC CAC	702
N D F D A I K K L I N D D T K K D M	252
AAC GAT TTC GAC GCA ATC AAA AAG TTG ATC AAC GAC GAT ACT AAG AAA GAC ATG	756
L G K L L S T G L V Q N F P N T I I	270
CTT GGA AAA CTG CTG TCG ACA GGC TTG GTC CAA AAC TTC CCG AAC ACC ATT ATA	810
S K L I E G K F Q D M L N I S Q H Q	288
AGC AAG CTG ATC GAA GGA AAG TTT CAG GAT ATG CTG AAC ATC TCT CAG CAT CAA	864
C V K K Q C P E N S G C F R H L D E	306
TGC GTG AAG AAG CAA TGT CCC GAG AAT TCA GGT TGC TTC CGC CAC TTA GAC GAA	918
R E E C K C L L N Y K Q E G D K C V	324
AGG GAG GAA TGT AAA TGC CTG CTG AAT TAT AAA CAG GAA GGA GAC AAG TGC GTA	972
E N P N P T C N E N N G G C D A D A	342
GAG AAT CCT AAC CCA ACC TGT AAC GAA AAT AAC GGT GGC TGC GAT GCT GAC GCT	1026
K C T E E D S G S N G K K I T C E C	360
AAG TGT ACC GAG GAG GAC AGC GGT TCC AAT GGC AAG AAA ATA ACT TGC GAA TGC	1080
T K P D S Y P L F D G I F C S H D E	378
ACG AAG CCC GAT AGT TAC CCT CTC TTC GAC GGT ATC TTC TGC TCC CAT GAT GAG	1134
L * E L T	383
CTT TAA GAG CTC ACC	

Fig. 8

10098544-03102

R I Q G D I T M D N I L S G F E N E	18
CGG ATC CAA GGA GAT ATA ACA ATG GAC AAC ATC CTC AGT GGC TTC GAG AAC GAG	54
Y D V I Y L K P L A G V Y R S L K K	36
TAC GAC GTA ATC TAC CTA AAG CCC CTT GCC GGT GTC TAC CGT TCA TTG AAG AAA	108
Q I E K N I F T F N L N L N D I L N	54
CAG ATA GAA AAG AAT ATT TTC ACG TTC AAC CTC AAC CTA AAT GAC ATC CTC AAC	162
S R L K K R K Y F L D V L E S D L M	72
TCG CGC CTC AAG AAG CGA AAA TAC TTC CTC GAC GTG TTG GAA TCC GAC CTT ATG	216
Q F K H I S S N E Y I I E D S F K L	90
CAA TTC AAG CAC ATT AGC TCT AAC GAG TAC ATC ATA GAG GAC AGC TTC AAG CTC	270
L N S E Q K N T L L K S Y K Y I K E	108
TTG AAT TCA GAA CAG AAG AAC ACC CTC CTA AAG TCC TAC AAA TAC ATT AAG GAG	324
S V E N D I K F A Q E G I S Y Y E K	126
TCT GTT GAG AAC GAC ATC AAG TTC GCC CAG GAA GGA ATT AGC TAC TAT GAG AAA	378
V L A K Y K D D L E S I K K V I K E	144
GTC CTG GCT AAA TAC AAG GAC GAC TTG GAA AGC ATT AAG AAG GTA ATC AAA GAA	432
E K E K F P S S P P T T P P S P A K	162
GAG AAG GAA AAG TTT CCG AGC TCT CCA CCC ACA ACT CCC CCA TCG CCT GCA AAG	486
T D E Q K K E S K F L P F L T N I E	180
ACC GAC GAG CAG AAA AAA GAA AGT AAG TTC CTT CCA TTC CTC ACC AAC ATC GAA	540
T L Y N N L V N K I D D Y L I N L K	198
ACT CTA TAT AAC AAC CTG GTG AAC AAG ATT GAT GAC TAC TTA ATC AAC TTG AAG	594
A K I N D C N V E K D E A H V K I T	216
GCG AAA ATT AAT GAC TGT AAC GTC GAA AAG GAT GAA GCC CAC GTT AAG ATC ACC	648
K L S D L K A I D D K I D L F K N H	234
AAG CTT TCC GAT CTC AAA GCC ATC GAC GAT AAG ATT GAC CTG TTT AAG AAC CAC	702
N D F D A I K K L I N D D T K K D M	252
AAC GAT TTC GAC GCA ATC AAA AAG TTG ATC AAC GAC GAT ACT AAG AAA GAC ATG	756
L G K L L S T G L V Q N F P N T I I	270
CTT GGA AAA CTG CTG TCG ACA GGC TTG GTC CAA AAC TTC CCG AAC ACC ATT ATA	810
S K L I E G K F Q D M L N I S Q H Q	288
AGC AAG CTG ATC GAA GGA AAG TTT CAG GAT ATG CTG AAC ATC TCT CAG CAT CAA	864
C V K K Q C P E N S G C F R H L D E	306
TGC GTG AAG AAG CAA TGT CCC GAG AAT TCA GGT TGC TTC CGC CAC TTA GAC GAA	918
R E E C K C L L N Y K Q E G D K C V	324
AGG GAG GAA TGT AAA TGC CTG CTG AAT TAT AAA CAG GAA GGA GAC AAG TGC GTA	972
E N P N P T C N E N N G G C D A D A	342
GAG AAT CCT AAC CCA ACC TGT AAC GAA AAT AAC GGT GGC TGC GAT GCT GAC GCT	1026
K C T E E D S G S N G K K I T C E C	360
AAG TGT ACC GAG GAG GAC AGC GGT TCC AAT GGC AAG AAA ATA ACT TGC GAA TGC	1080
T K P D S Y P L F D G I F C S H D E	378
ACG AAG CCC GAT AGT TAC CCT CTC TTC GAC GGT ATC TTC TGC TCC CAT GAT GAG	1134
L * E L T	383
CTT TAA GAG CTC ACC	1149

Fig 9

Fig 10

DNA AND AMINO ACID SEQUENCE OF BVp42-M

attggatccactaaa

13 atgtggtccttggaagtgtcttttattctgggctgtccttggtgacc
M W S W K C L L F W A V L V T
58 gccactctttgcacagcagcgatctctgttactatggacaacatc
A T L C T A A I S V T M D N I
103 ctcagtggcttcgagaacgagtagcagcgtaatctacctaagccc
L S G F E N E Y D V I Y L K P
148 cttgccggtgtctaccgttcattgaagaaacagatagaaaagaat
L A G V Y R S L K K Q I E K N
193 attttcacgttcaacctcaacctaaatgacatcctcaactcgcgc
I F T F N L N L N D I L N S R
238 ctcaagaagcgaaaatacttcctcgacgtgttggaatccgacctt
L K K R K Y F L D V L E S D L
283 atgcaatttaagcacattagctctaacgagtagcatcatagaggac
M Q F K H I S S N E Y I I E D
328 agcttcaagctcttgaattcagaacagaagaacaccctcctaag
S F K L L N S E Q K N T L L K
373 tcctacaaatacattaaggagtctgttgagaacgacatcaagttc
S Y K Y I K E S V E N D I K F
418 gccaggaaggaattagctactatgagaaagtcctggctaataac
A Q E G I S Y Y E K V L A K Y
463 aaggacgacttggaagcattaagaaggtaatcaaagaagagaag
K D D L E S I K K V I K E E K
508 gaaaagtttccgagctctccaccacaactccccatcgctgca
E K F P S S P P T T P P S P A
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K T D E Q K K E S K F L P F L
598 accaacatcgaaactctatataacaacctggtgaacaagattgat
T N I E T L Y N N L V N K I D
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D Y L I N L K A K I N D C N V
688 gaaaaggatgaagcccacgttaagatcaccaagctttccgatctc
E K D E A H V K I T K L S D L
733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat
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100954-01102

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 C L L N Y K Q E G D K C V E N
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 P N P T C N E N N G G C D A D
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 I F C S

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